Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci

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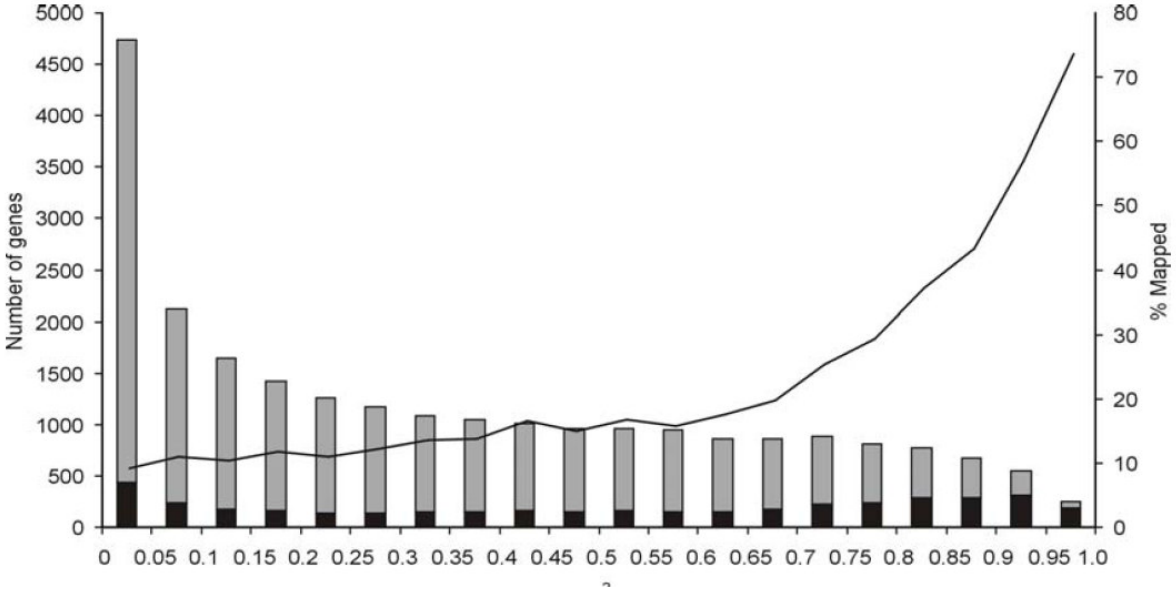

Fig. 3. Frequency distribution of heritability values of gene expression in a microarray comparison of the parents. Black and gray bars represent the number of genes that could and could not be mapped, respectively. The solid line depicts the number of mapped genes as a proportion of the total number of genes for a given heritability class.

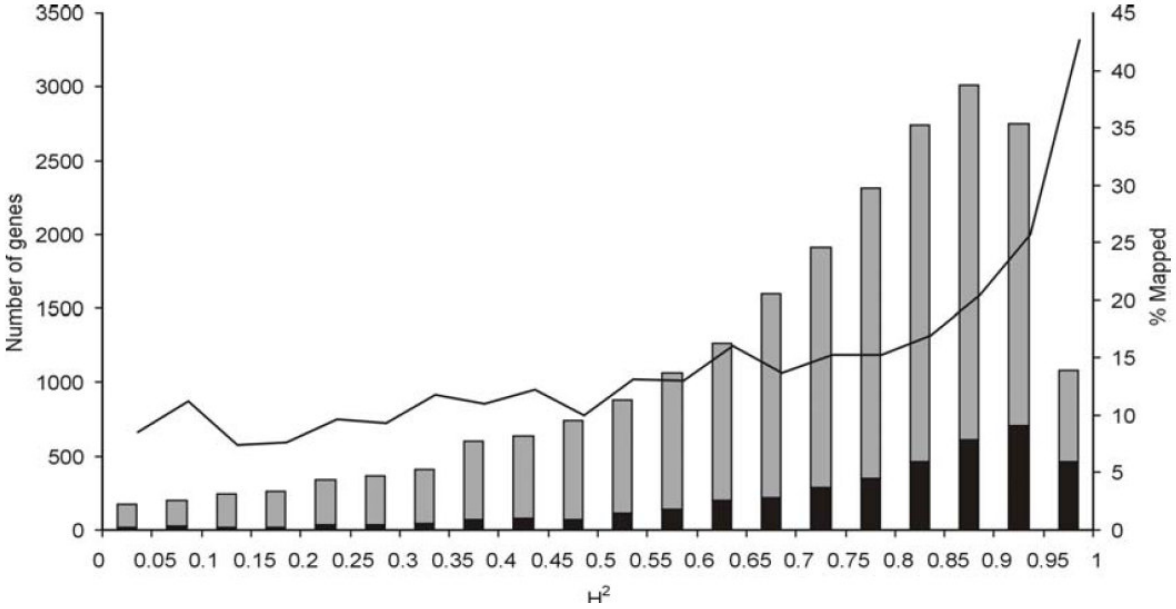

Fig. 4. Frequency distribution of heritability values of gene expression in a microarray analysis of the Cvi × L*er* RIL population. Black and gray bars represent the number of genes that could and could not be mapped, respectively. The solid line depicts the number of mapped genes as a proportion of the total number of genes for a given heritability class.

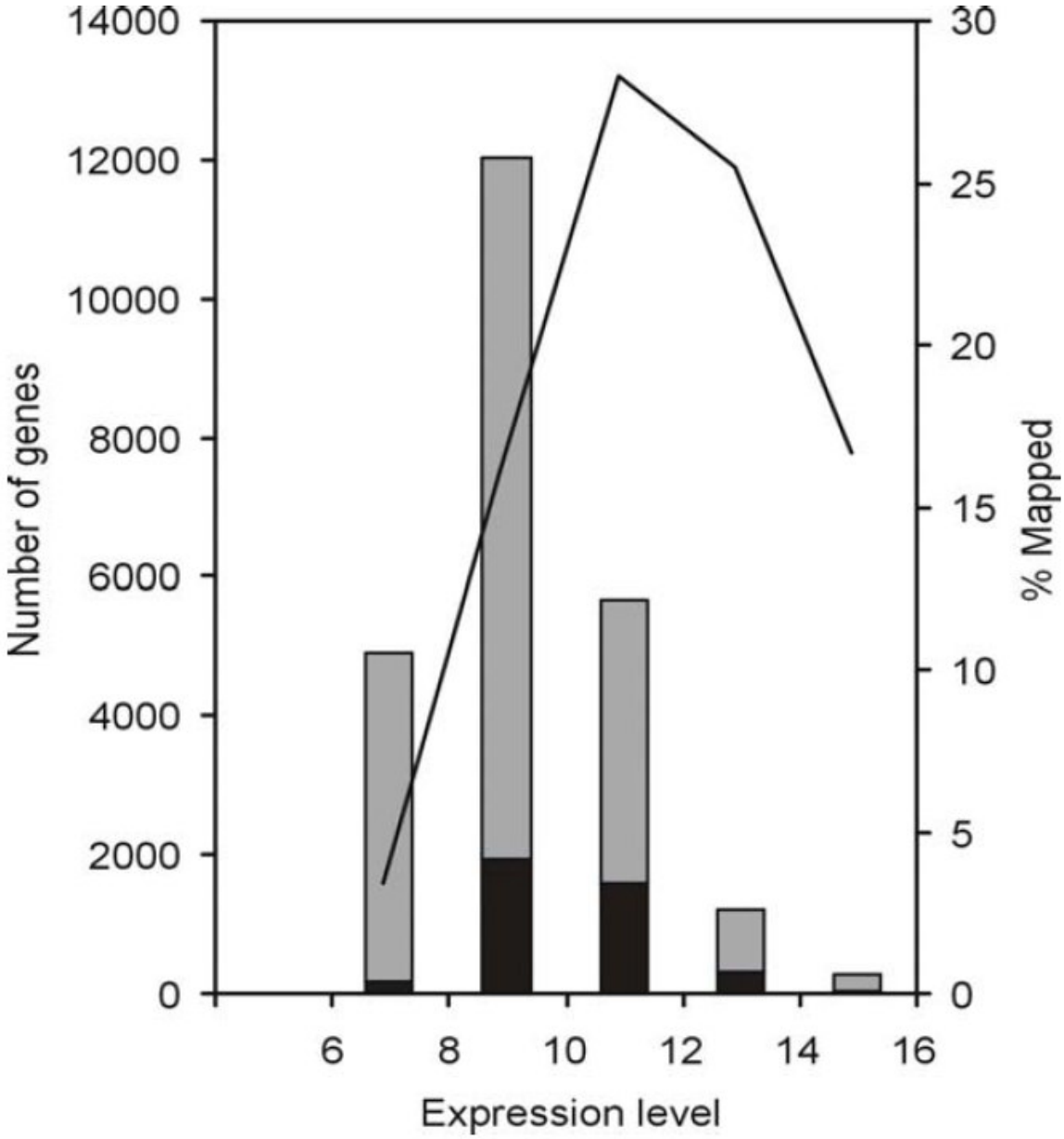

Fig. 5. Frequency distribution of the mean expression level of analyzed genes in the RIL population. Black and gray bars represent the number of genes that could and could not be mapped, respectively. The solid line depicts the number of mapped genes as a proportion of the total number of genes for a given class.

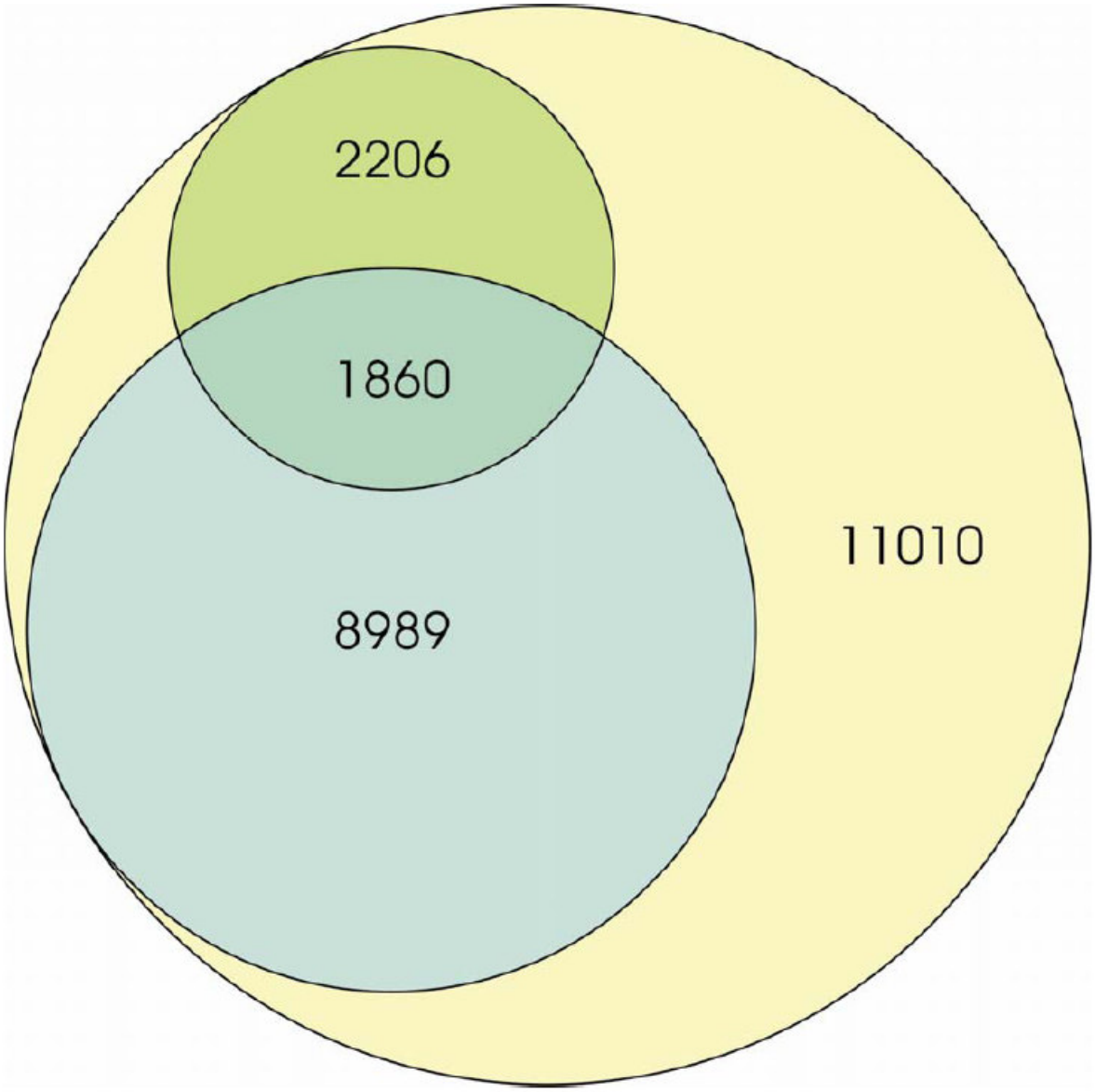

Fig. 6. Diagram of the number of genes showing linkage and transgression. Circles are proportional to the number of genes. The diagram is color coded as follows: yellow, the total number of genes analyzed (24,065); green, the number of genes whose expression showed significant linkage (4,066); blue, the number of genes whose expression showed transgressive segregation (10,849).

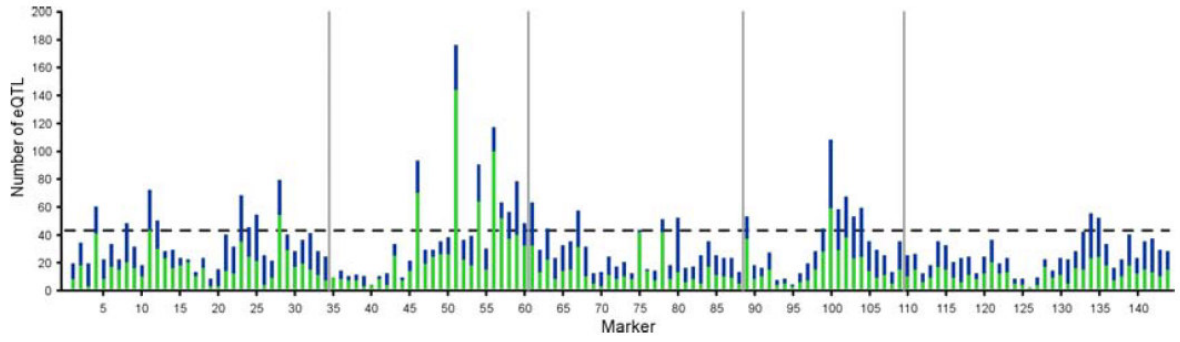

Fig. 7. Genomic distribution of eQTLs. Bars represent the number of distant (green) and local (blue) eQTLs detected at each marker position. Each eQTL was positioned at its best controlling marker. The dashed horizontal line represents the significance threshold value for defining a hot spot. Gray vertical lines depict chromosomal borders.

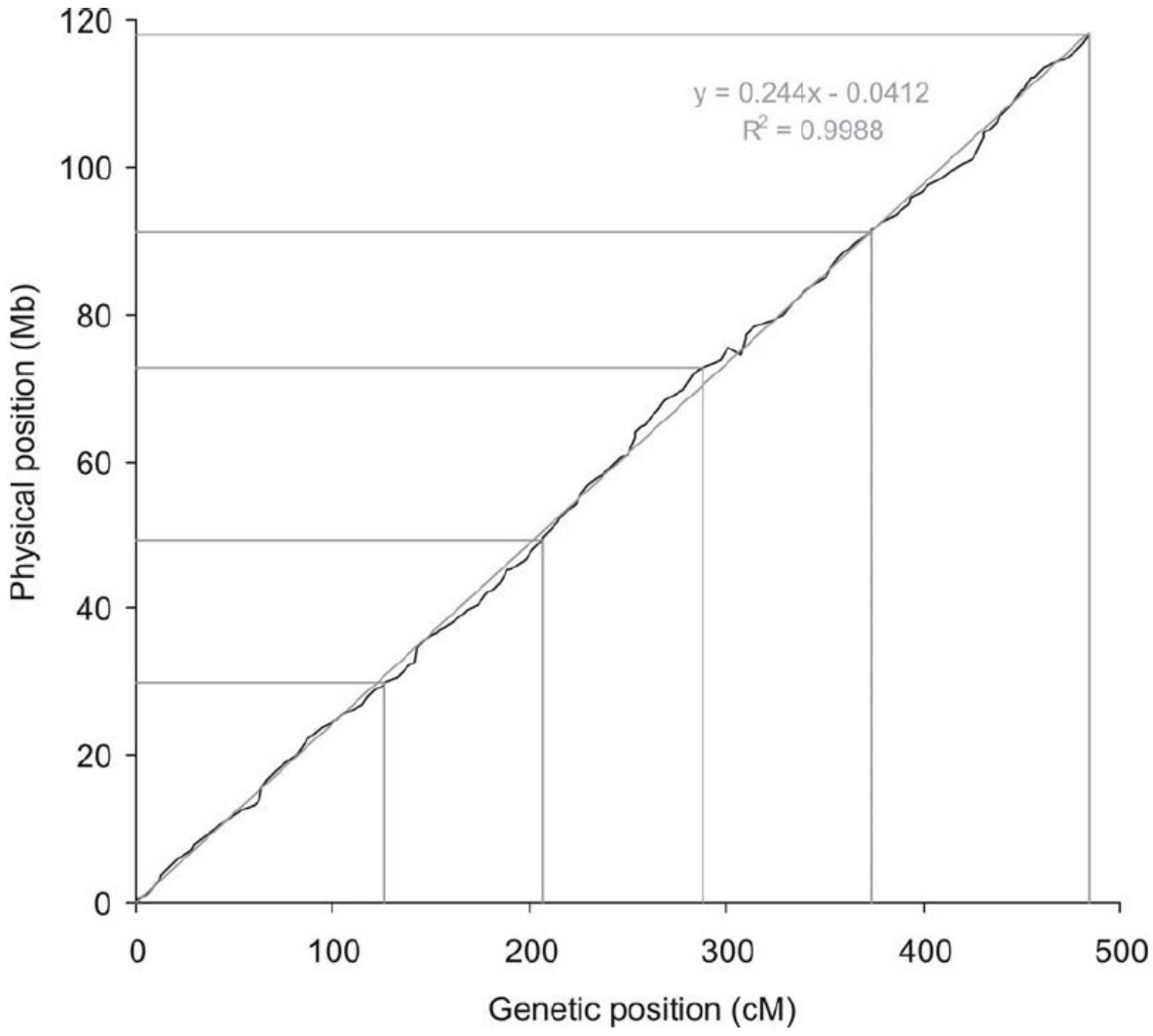

Fig. 8. Relationship between genetic and physical positions on the *Arabidopsis* genome. Horizontal and vertical gray lines represent chromosomal borders. The diagonal gray line depicts the average relation based on regression analysis.

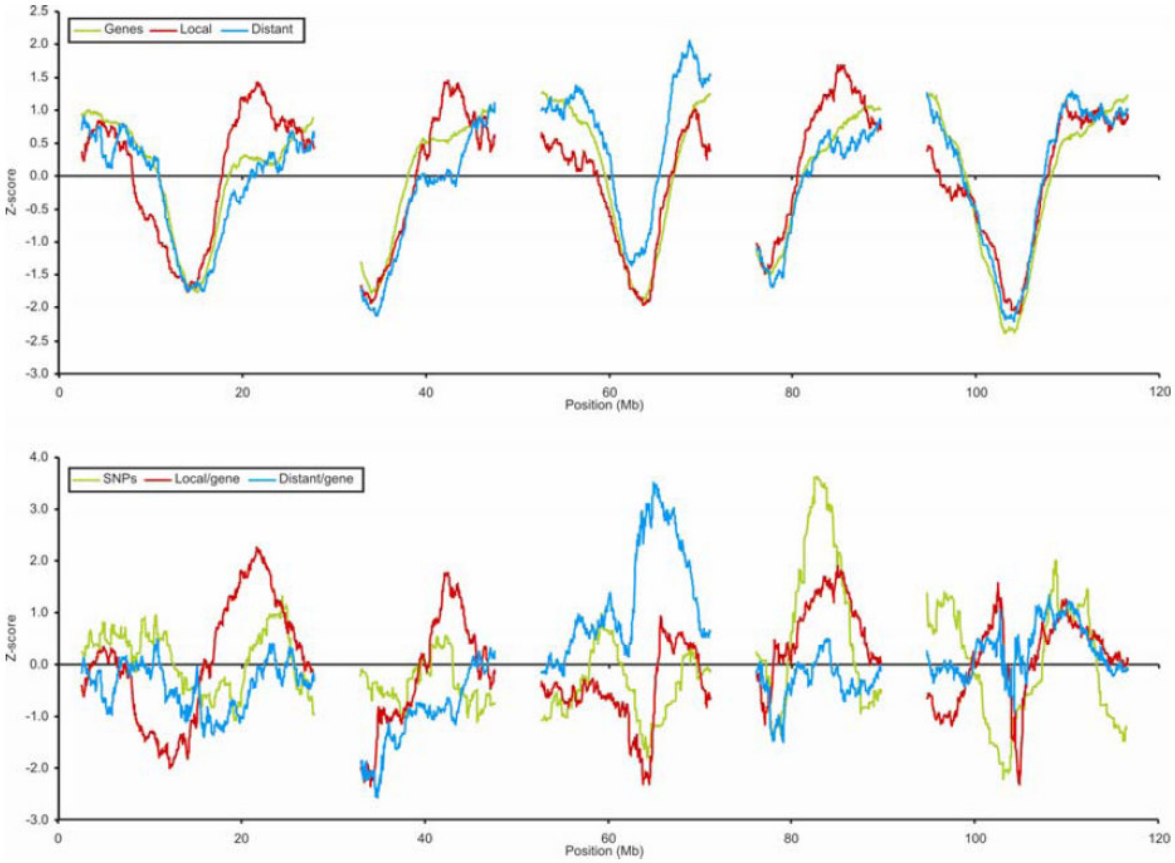

Fig. 9. Relation between gene and SNP frequency and the number of mapped genes. (*Upper*) The relation between gene frequency and the number of mapped genes, divided in locally and distantly regulated genes. (*Lower*) The relation between SNP frequency and the number of mapped genes divided in locally and distantly regulated genes and corrected for gene density.

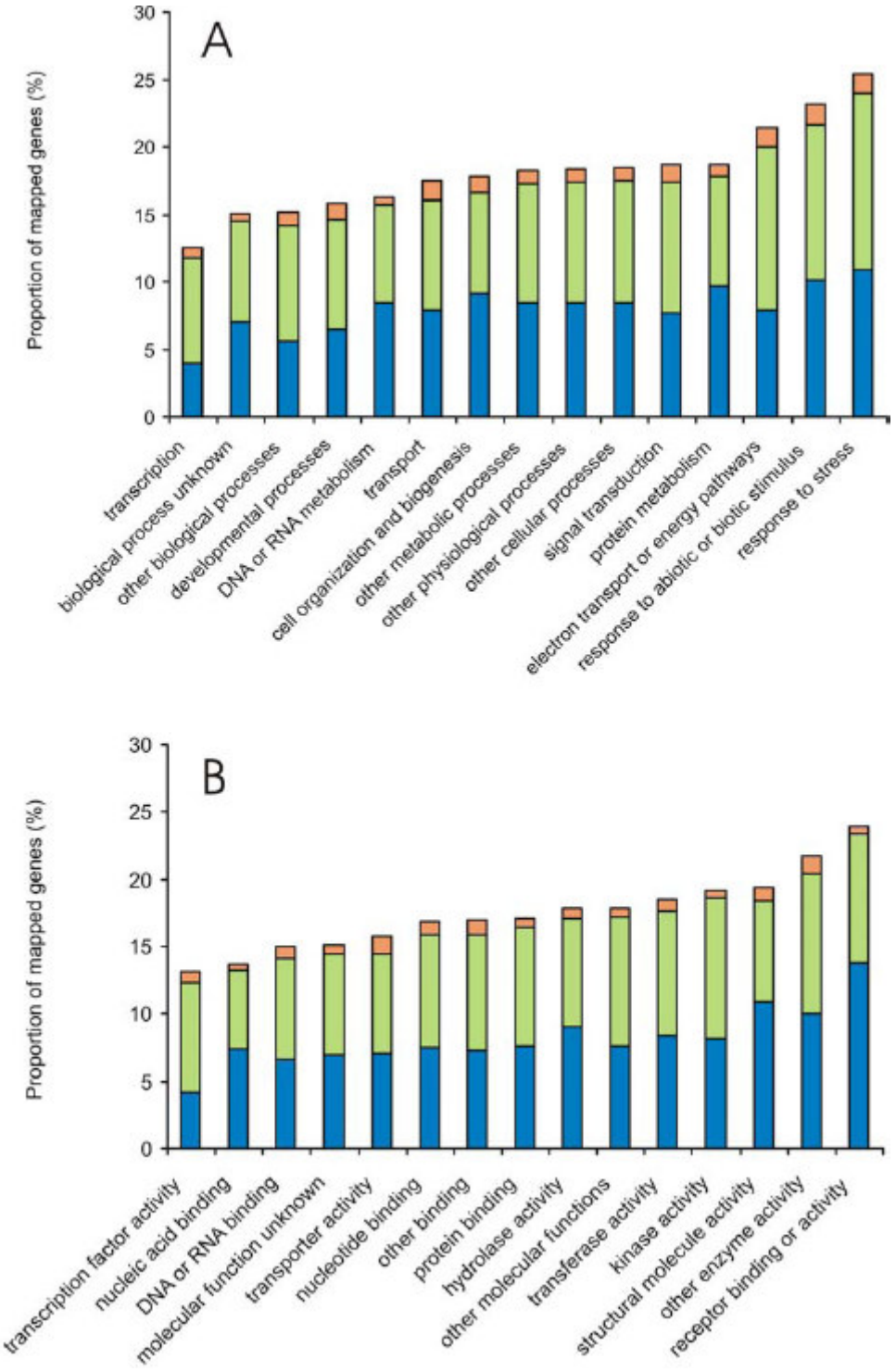

Fig. 10. Frequency distribution of the proportion of mapped genes versus function. (*A*) Proportion of genes that could be mapped in different functional classes. (*B*) Proportion of genes that could be mapped in different classes of molecular function. The graphs are color-coded as follows: blue, local regulation; green, distant regulation; orange, both local and distant regulation.